uncontrolled growth; and [,]

(c) comparing the CT-1 expression level in the test cells with the expression level in the control cells, wherein a higher expression level in the test sample indicates the presence of tumor in the mammal [from which the test tissue cells were obtained].

Please cancel claim 2 without prejudice to later prosecution.

3. (Amended) The method of claim [2] 1 wherein said test sample is obtained from an individual suspected to have neoplastic cell growth or proliferation.

Please cancel claims 4-23 without prejudice to later prosecution.

Please add the following new claims:

--24. The method of claim 3 wherein the test sample is from a human.

25. The method of claim 1 wherein the ~~CT-1~~ expression level in the test sample cells is at least two-fold greater than in the control cells.

26. The method of claim 1 wherein the test sample is from cancerous tissue.

27. The method of claim 26 wherein the cancerous tissue is selected from the group consisting of breast cancer, prostate cancer, colon cancer, squamous cell cancer, small-cell lung cancer, non-small-cell lung cancer, gastrointestinal cancer, pancreatic cancer, glioblastoma, cervical cancer, ovarian cancer, liver cancer, bladder cancer, hepatoma, colorectal cancer, endometrial cancinoma, salivary gland carcinoma, kidney cancer, vulval cancer, thyroid cancer, and head and neck carcinoma.

28. A method of diagnosing tumor in a mammal, the method comprising:

(a) detecting the number of copies of a gene encoding a cardiotrophin-1 (CT-1) polypeptide in a test sample of tissue cells obtained from the mammal, wherein the cells are suspected of uncontrolled growth and wherein the detecting is by contacting, under stringent conditions, nucleic acid of the test sample cells

with
a nucleic acid probe comprising at least 20 contiguous nucleic acid bases from DNA 58125 (SEQ ID NO:1) or its complement (SEQ ID NO:2);

(b) detecting the number of copies of a nucleic acid marker sequence on the chromosome encoding a cardiotrophin-1 (CT-1) polypeptide in the test sample, which marker gene is not amplified; and

(c) comparing the CT-1 gene copy number in the test cells with the gene copy number of the marker gene, wherein a higher CT-1 gene copy number indicates the presence of tumor in the mammal.

B3 Cont.

29. The method of claim 28 wherein the marker sequence is detected by contacting, under stringent conditions, nucleic acid of the test sample with a nucleic acid marker probe comprising at least 20 contiguous nucleic acid bases from a sequence, or its complement, in Chromosome 16 from chromosomal regions selected from the group consisting of regions P7, P55, P89, P90, P92, P93, P94, P95, P99, P154, and P208.

30. The method of claim 29 wherein the marker probe is selected from the group consisting of Stanford Human Genome Center Marker Probes SHGC-2835, SHGC-9643, SHGC-11302, EST00087, SHGC-2726, SHGC-361232, SHGC-35326, IB391, GATA7B02, SHGC-33727, and SHGC-13574.

31. The method of claim 28 wherein said test sample is obtained from an individual suspected to have neoplastic cell growth or proliferation.

32. The method of claim 31 wherein the test sample is from a human.

Sub C12

33. The method of claim 26 wherein the CT-1 copy number in the test sample cells is at least two-fold greater than the copy number of unamplified marker sequences.

34. The method of claim 28 wherein the test sample is from cancerous tissue.

Sub C13

35. The method of claim 28 wherein the cancerous tissue is selected from the group consisting of breast cancer, prostate cancer, colon cancer, squamous cell cancer, small-cell lung cancer, non-small-cell lung cancer, gastrointestinal cancer, pancreatic cancer, glioblastoma, cervical cancer, ovarian cancer, liver cancer,